

Figure 1.

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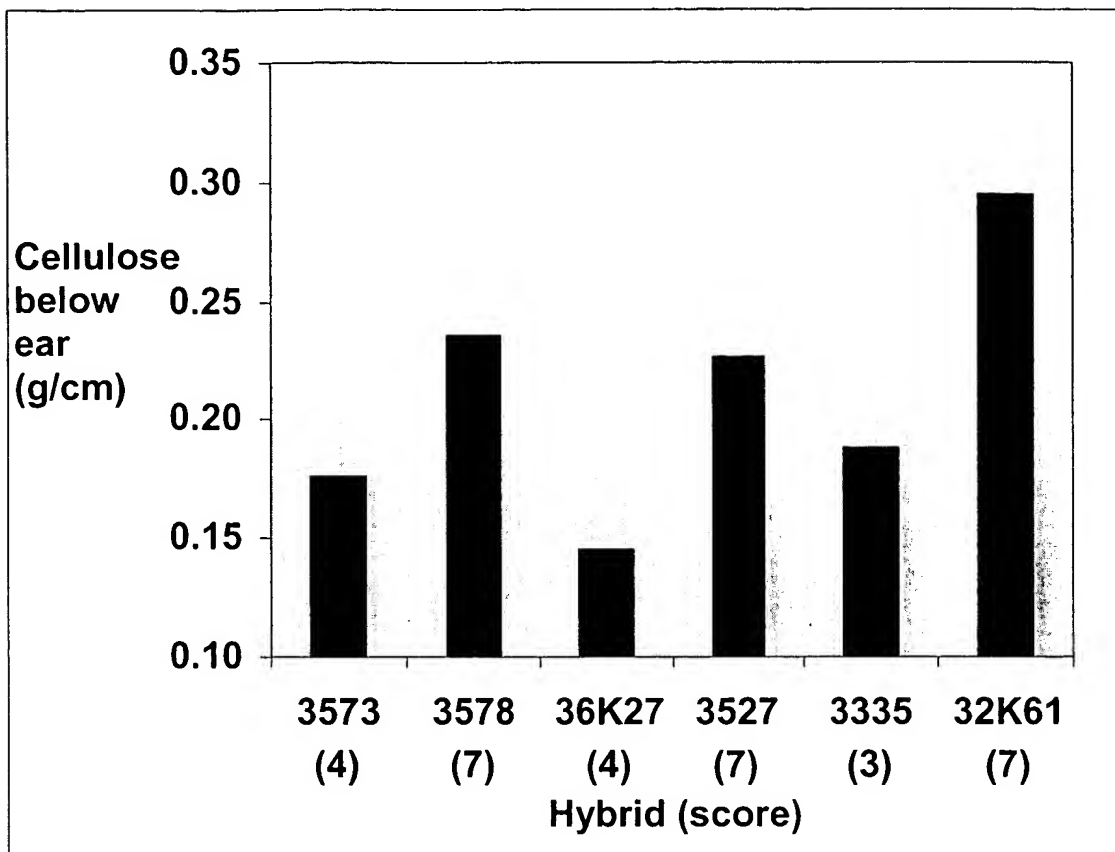


Figure 2.

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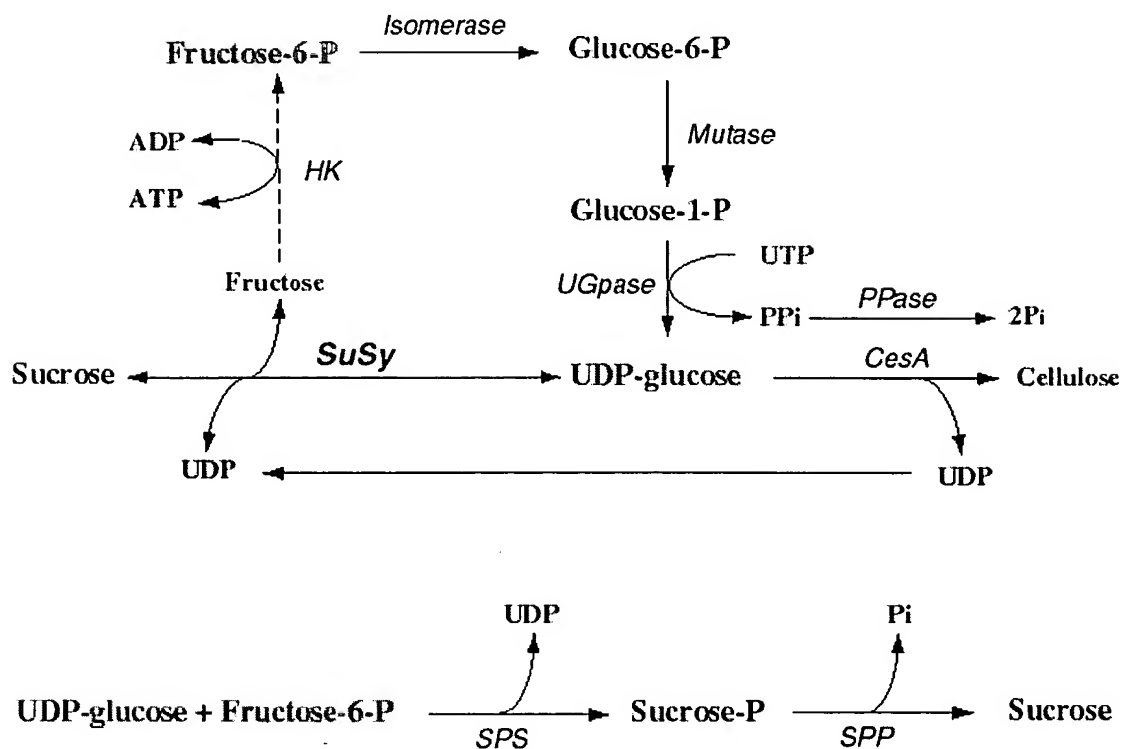


Figure 3.

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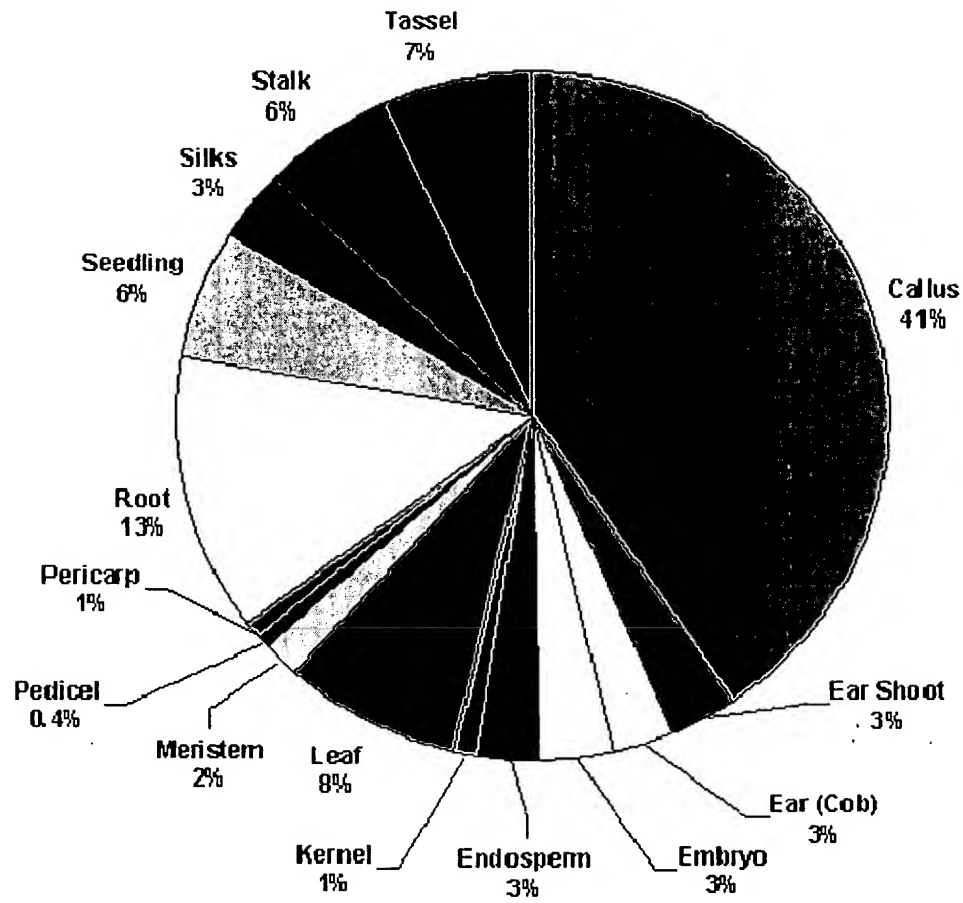


Figure 4.

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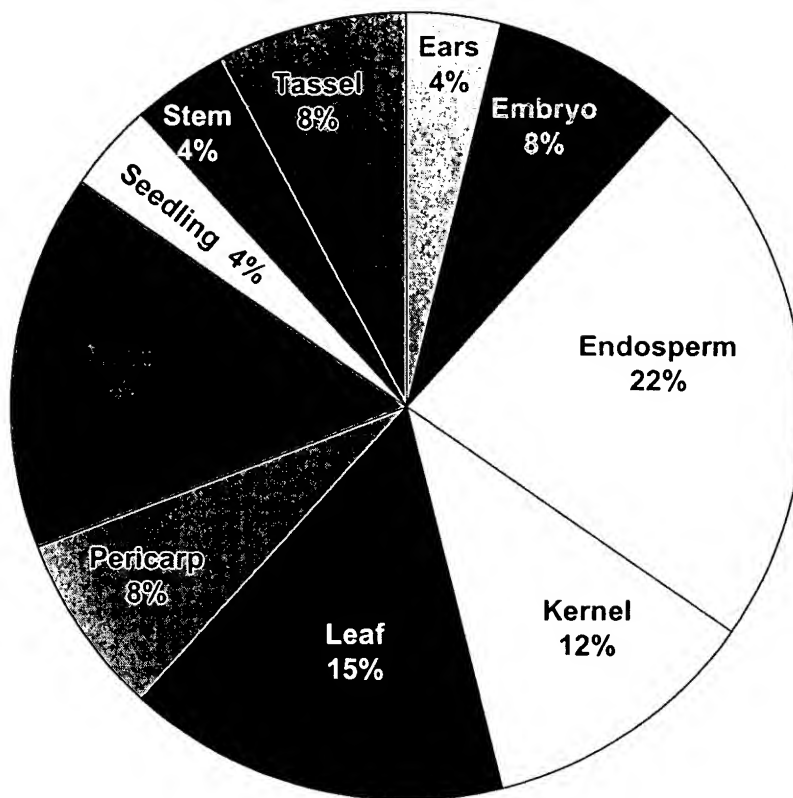


Figure 5

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Allele 1: CACCCGG-mu-AGATTG

Allele 2: CACC-mu-CGGAGATTG

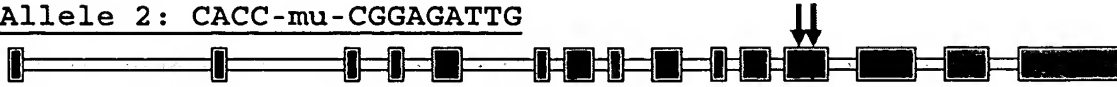


Figure 6.

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Genotype	structural dry matter (% of total dry matter)	cellulose (% of total dry matter)	cellulose (% of structural dry matter)
<i>Sus-1</i> (WT)	63.2	25.2 +/-0.38	39.9
<i>sus-1</i> (mutant)	47.3	17.7 +/-0.34	37.4

Figure 7.

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		1	50
Sh1	(1)	-----MAAKLTRLHSLRERLGATFSSHPNELIALFSRYVHQGKGMQRHQ	
Sus1	(1)	MGEAGADRVLSRLHSVRERIGDSL SAHPNELVAVFTRLKNLGKGMQPHQ	
Sus3	(1)	-----STHASGDRVEDTLHAHRNELVALLSKYVNGKKGILQPHH	
Consensus	(1)	LSRLHSLRERIGDTLSAHPNELVALFSRYVN GKGMLQPHQ	
		51	100
Sh1	(46)	LLAEFD-ALFDSDE--KYAPFEDILRAAQEAIVLPPWVALAIRPRPGVW	
Sus1	(51)	IIAEYNNATPEAEREKLKDGAFEDVLRAAQEAIVIPPWVALAIRPRPGVW	
Sus3	(40)	ILDALDEVQSGGGA-LAEGPFLDVLRS AQEAIVLPPFVAIAVRPRPGVW	
Consensus	(51)	ILAEFD AI DADRE LKDGPFEDVLRAAQEAIVLPPWVALAIRPRPGVW	
		101	150
Sh1	(93)	DYIRVNVSELAVEELSVSEYLA FKEQLVDGQSNFVLELDFEFPNASFP	
Sus1	(101)	EYVRVNVSELAVEELRVPEYLQFKEQLVEEGPNNNFVLELDFEFPNASFP	
Sus3	(89)	EYVRVNVHEL SVEQLTVSEYLR FKEELVDGQHNDPYVLELDFEFPNVSVF	
Consensus	(101)	EYVRVNVSELAVEELSVSEYL FKEQLVDGQ N NFVLELDFEFPNASFP	
		151	200
Sh1	(143)	RPSMSK SIGNGVQFLNRHLSSKLFQDKESLYPLLNF LKAHNYKGTMMMLN	
Sus1	(151)	RPSLSK SIGNGVQFLNRHLSSKLFHDKESMYPLLNF LRAHNYKGMTMMMLN	
Sus3	(139)	RPNRSS SIGNGVQFLNRHLSSIMFRNRDCLEPLLD FLRGHRHKGHVMMMLN	
Consensus	(151)	RPSLSK SIGNGVQFLNRHLSSKLF DKESLYPLLNF LRAHNYKG TMMMLN	
		201	250
Sh1	(193)	DRIQSLRGLQSSLRKAE EYLLSVPQDTPYSEFNHRFOELGLEKGWGD TAK	
Sus1	(201)	DRIRSL SALQGALRKAE EHLSTLQADTPYSEFHHRFOELGLEKGWGDCAK	
Sus3	(189)	DRIQSLGR LQSVLT KAE EHL SKLPADTPYSQFAYKFQEWGLEKGWGD TAG	
Consensus	(201)	DRIQSL ALQSALRKAE EHLSSLPADTPYSEF HRFQELGLEKGWGD TAK	
		251	300
Sh1	(243)	RVLDTLHLLLDLLEAPDPANLEKFLGTIPMMFN VVILSPHG YFAQSNVLG	
Sus1	(251)	RAQETIHLLLDLLEAPDPSTLEKFLGTIPMFVFN VVILSPHG YFAQANVLG	
Sus3	(239)	HVLEMIHLLLDI IQADPSTLEKFLGRIPMIFN VVVVSPHG YFGQANVLG	
Consensus	(251)	RVLETIHLLLDLLEAPDPSTLEKFLGTIPMIFN VVILSPHG YFAQANVLG	
		301	350
Sh1	(293)	YPDTGGQV VYILDQVRAL ENEMLLRIKQ QGLDITPKILIVTRLLPDA GT	
Sus1	(301)	YPDTGGQV VYILDQVRAM ENEMLLRIKQ CGLDITPKILIVTRLLPDA GT	
Sus3	(289)	LPDTGGQI VYILDQVRAL ENEMVLR LKQGLDVSPKILIVTRLLPDA GT	
Consensus	(301)	YPDTGGQV VYILDQVRAL ENEMLLRIKQ QGLDITPKILIVTRLLPDA GT	
		351	400
Sh1	(343)	TCGQRLEKVIGTEHTDI IRVPFRNENGILRKWIS RFDVWPYLETYTEDVS	
Sus1	(351)	TCGQRLEKVLGTEHCHILRV PFRTENGIVRKWIS RFEVWPYLETYTD DVA	
Sus3	(339)	SCNQRLE R ISGTQHTYILRV PFRNENGILKKWIS RFDVWPYLETFAEDAA	
Consensus	(351)	TCGQRLEKVIGTEHTHILRV PFRNENGILRKWIS RFDVWPYLETYTEDVA	
		401	450
Sh1	(393)	SEIMKEMQAKPDLIIGNYSDGNLVATLLAHKLGVT OCTIAHALEKTKYPN	
Sus1	(401)	HEIAGELQANPDLIIGNYSDGNLVACLLAHKMGVT HCTIAHALEKTKYPN	
Sus3	(389)	GEIAAELQGT PDIIGNYSDGNLVASLLSYKMGIT QCNIAHALEKTKYPD	
Consensus	(401)	EIAAELQA PDLIIGNYSDGNLVASLLAHKMGVT QCTIAHALEKTKYPN	
		451	500
Sh1	(443)	SDIYLDKFDSQYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKD TVGQYE	
Sus1	(451)	SDLYWKKFEDHYHFSCQFTTDLIAMNHADFIITSTFQEIAGNKD TVGQYE	
Sus3	(439)	SDIFWKNFDEKYHFSCQFTADLIAMNHADFIITSTYQEIAGSKN TVGQYE	
Consensus	(451)	SDIYWKKFDD YHFSCQFTADLIAMNHADFIITSTFQEIAGSKD TVGQYE	
		501	550
Sh1	(493)	SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSVYYPYTETDKRLTAFH	
Sus1	(501)	SHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADLSIYFPYTESHKRLTSLH	
Sus3	(489)	SHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPHTEKAKRLTSLH	
Consensus	(501)	SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTES KRLTSLH	

Figure 8a

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		551		600
Sh1	(543)	PEIEELIYSDVENSEHKFVLKDKKKPIIFSMARLDRVKNMTGLVEMYGKN		
Sus1	(551)	PEIEELLYSQTEHTEHKFVLNDRNKPIIFSMARLDRVKNLTGLVELYGRN		
Sus3	(539)	GSIENTLIYDPEQNDHIGHLDRSKPILFSMARLDRVKNITGLVEAFKAC		
Consensus	(551)	PEIEELIYS ENSEHKFVL DR KPIIFSMARLDRVKNITGLVELYGKN		
		601		650
Sh1	(593)	ARLRELANLVIVAGDHGK-ESKDREEQAEFFKMYSLIDEYKLGHIRWIS		
Sus1	(601)	KRLQELVNLVVVCGDHGN-PSKDKEEQAEFFKMFDLIEQYNLNGHIRWIS		
Sus3	(589)	AKLRELVLNVLVVVAGYNDVNKSKDREEIAEIEKMHELKTHNLFQFRWIS		
Consensus	(601)	ARLRELVLNVLVVVAGDHG SKDREEQAEFFKMHDLID YNL GHIRWIS		
		651		700
Sh1	(642)	AQMNRVRNGELYRYICDTKGAFVQPAFYEAFLTVIESMTCGLPTIATCH		
Sus1	(650)	AQMNRVRNGELYRYICDTKGAFVQPAFYEAFLTVVEAMTCGLPTFATAY		
Sus3	(639)	AQTNRARNGELYRYIADTHGAFVQPALYEAFLTVVEAMTCGLPTFATLH		
Consensus	(651)	AQMNRVRNGELYRYICDTKGAFVQPAFYEAFLTVVEAMTCGLPTFAT H		
		701		750
Sh1	(692)	GGPAEIIIVDGVSGLHIDPYHSDKAADILVNFFDKCKADPSYWDEISQGGI		
Sus1	(700)	GGPAEIIIVHGVSGYHIDPYQGDKASALLVDFFDKCOAEP SHWSKISQGGI		
Sus3	(689)	GGPAEIIIEHGVSGFHIDPYHPEQAVNLMADFFDRCKQDPDHVWNISGAGI		
Consensus	(701)	GGPAEIIIVHGVSGFHIDPYH DKAALVDFFDKCKADPSHW ISQGGI		
		751		800
Sh1	(742)	QRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYIEMFYALKYR		
Sus1	(750)	QRIEEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMLYALKYR		
Sus3	(739)	QRIYEKYTWKIYSERLMTLAGVYGFWKYVSKLERLETRRYLEMFYILKFR		
Consensus	(751)	QRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMFYALKYR		
		801		817
Sh1	(792)	SLASQVPLSFD-----		
Sus1	(800)	TMASTVPLAVEGEPSSK		
Sus3	(789)	ELAKTVPLAID-QPQ--		
Consensus	(801)	SLASTVPLAID P		

Figure 8b

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		1	50
Sh1	(1)	AAACCTCCCTCCCTCCTCCATTGGA	CTGCTTGCTCCCTGTTGACCATTG
Sus1	(1)	-----GCCTGAG-GATCCAGGAAGAGGACAG	
Sus3	(1)	-----	
Consensus	(1)	G CTG G TCC G GA A G	
		51	100
Sh1	(51)	GGTATTCTGAACCATCGAGCCATGGCTGCCAAGCTGACTCGCCTTCACAG	
Sus1	(26)	CA-ATGGGGGAAGGTGCAGGTGACCGTGTC--CTGAGCCGCCTCCACAG	
Sus3	(1)	-----GTCGAC-CCACGC	
Consensus	(51)	AT G A T AG TG C CTGAGTCGCCTCCACAG	
		101	150
Sh1	(101)	TCCTCGCGAACGCCTTGGTGCCACCTTCTCCTCCCATCCCAATGAACTGA	
Sus1	(72)	CGTCAGGGAGCGCATTGGCGACTCACTCTCTGCCACCCCAATGAGCTTG	
Sus3	(13)	GTCCGGCGACCGCGTCGAGGACACCTCCACGCGCACCGCAACGAGCTCG	
Consensus	(101)	TC GCGA CGC TTGG GACACCTCTCCGCCCCACCCCAATGAGCT G	
		151	200
Sh1	(151)	TAGCACTCTTTTCCAGGTATGTTCAACAGGGCAAGGGAATGCTTCAGCGC	
Sus1	(122)	TCGCCGTCTTCACCAGGCTGAAAAACCTTGAAAGGGTATGCTGCAGCCC	
Sus3	(63)	TCGCCCTCTGTCCAAGTACGTGAACAAGGGGAAGGGCATCTGCAGCCG	
Consensus	(151)	TCGCCCTCTT TCCAGGTA GT AACCAGGG AAGGG ATGCTGCAGCCC	
		201	250
Sh1	(201)	CATCAGCTGCTTGCGGAGTTTGA--TGC---CCTGTT--TGATAGTGA	
Sus1	(172)	CACCAGATCATTGCCGAGTACAACAATGCGATCCCTGAGGCTGAGCGGA	
Sus3	(113)	CACCAATCCTCGACGCGCTCGACGAGGT---CCAGGG-CTCCGGGGGC	
Consensus	(201)	CACCAGATCCTTGCCGAGTTCGAC ATGC CCTG G CTGAG G GA	
		251	300
Sh1	(242)	CAAGGAGAAG--TATGCACCATTTGAAGACATTCTTCGTGCTGCTCAGGA	
Sus1	(222)	GAAGCTCAAG--GATGGTGCTTTTGAGGATGTCCTGAGGGCAGCTCAGGA	
Sus3	(158)	CGCGCGCTAGCCGAGGGACCTTCTCTGACGTCCTCCGCTCCGCGCAGGA	
Consensus	(251)	CAAGC CAAG GATGGACC TTTGA GACGTCCT CG GC GCTCAGGA	
		301	350
Sh1	(290)	AGCAATTGTGCTCCCCCATGGGTTGCACTTGCTATCAGGCCAAGGCCTG	
Sus1	(270)	GGCGATTGTCAATCCCCCATGGGTTGCACTTGCCATCCGCCCTAGGCCTG	
Sus3	(208)	GGCGATCGTGCTGCCGCCGTTCTGTTGCCATCGCGGTGCGCCCGCGCCGG	
Consensus	(301)	GGCGATTGTGCTCCCCCATGGGTTGCACTTGC ATCCGCC AGGCCTG	
		351	400
Sh1	(340)	GTGTCTGGGATTACATTGGGGTGAATGTAAGTGAGCTGGCTGTGGAGGAG	
Sus1	(320)	GTGTCTGGGAGTATGTGAGGGTCAACGTCACTGAGCTCGCTGTGAGGAG	
Sus3	(258)	GAGTTTGGGAGTACGTCCGCGTCAACGTTACGAGCTCAGCGTCGAGCAG	
Consensus	(351)	GTGTCTGGGAGTACGT CGGGTCAACGT AGTGAGCTCGCTGT GAGGAG	
		401	450
Sh1	(390)	CTGAGTGTTTCTGAGTACTTGGCATTCAAGGAACAGCTGGTGGATGGACA	
Sus1	(370)	CTGAGAGTTCTCTGAGTACCTGCAGTTCAAGGAACAGCTTGTGGAAGAAGG	
Sus3	(308)	CTCAGAGTCTCGGAGTACCTCCGCTTCAAGGAGGAGCTTGTGACGGCCA	
Consensus	(401)	CTGAGAGTTTCTGAGTACCTGC TTCAAGGAACAGCTTGTGGA GGACA	
		451	500
Sh1	(440)	ATCCAACAGCAACTTTGTGCTTGAGCTTGATTTTGAGCCCTTCAATGCCT	
Sus1	(420)	CCCCAACAACAACCTTTGTTCTTGAGCTGGACTTTGAGCCATTCAATGCCT	
Sus3	(358)	GCACAATGATCCCTACGTTCTCGAGCTTGACTTCGAGCCGTTCAATGTCT	
Consensus	(451)	CCCAACAACAACCTTTGTTCTTGAGCTTGACTTTGAGCC TTCAATGCCT	
		501	550
Sh1	(490)	CCTTTCTCGTCCTTCCATGTGCAAGTCCATCGGAAATGGAGTGCAATTC	
Sus1	(470)	CCTTCCCCGTCCTTCTCTGTCAAAGTCCATTGGCAATGGCGTGCAATTC	
Sus3	(408)	CAGTCCCACGCCCAATCGGTATCATCTATTGGAAACGGTGTGCAGTTC	
Consensus	(501)	CCTTCCC CGTCCTTCTCTGTCAAAGTCCATTGGAAATGG GTGCAGTTC	

Figure 9a

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		551	600
Sh1	(540)	CTTAACCGACACCTGTCTCAAGTTGTTCCAGGACAAGGAGAGTTTGTA	
Sus1	(520)	CTCAACAGGCACCTGTCTCAAAGCTCTTCCATGACAAGGAGAGCATGTA	
Sus3	(458)	CTCAACCGACACTTGTCTCAATCATGTTCCGCAACAGGGATTGCTTGG	
Consensus	(551)	CTCAACCGACACCTGTC TCAAAG TGTTCCA GACAAGGAGAGCTTGTA	
		601	650
Sh1	(590)	CCCCTTGCTGAACCTTCCTCAAGGCTCATAACTACAAGGGGCACGACGATGA	
Sus1	(570)	CCCCTTGCTCAACCTTCCTTCGCGCCCACTACAAGGGGATGACCATGA	
Sus3	(508)	GCCCCTGTTGGATTTCCTCCGTGGCCACCGGCACAAGGGGCATGTTATGA	
Consensus	(601)	CCCCTTGCTGAACCTTCCTCCG GCCCACAACCTACAAGGGGA GAC ATGA	
		651	700
Sh1	(640)	TGTTGAATGACAGAATCCAAAGCCTTCGTGGTCTCCAATCATCCCTGAGA	
Sus1	(620)	TGTTGAACGACAGAATCCGCACTCTCAGTGCTCTGCAAGGTGCGCTGAGG	
Sus3	(558)	TGCTTAATGATAGAATACAAAGCTTGGGGAGGCTTCAGTCTGTGCTGACC	
Consensus	(651)	TGTTGAATGACAGAATCCAAAGCCT GTGGTCT CAATCTGCGCTGAG	
		701	750
Sh1	(690)	AAGGCAGAGGAGTATCTACTGAGTGTTCCTCAAGACACTCCCTACTCGGA	
Sus1	(670)	AAGGCTGAGGAGCACCTGTCCACCCTACAAGCTGATACCCATACTCTGA	
Sus3	(608)	AAAGCTGAGGAGCACTTGTCAAGCTCCCTGCTGACACACCATACTCACA	
Consensus	(701)	AAGGCTGAGGAGCACCTGTC A CT CCTGCTGACAC CCATACTC GA	
		751	800
Sh1	(740)	GTTCAACCATAGGTTCCAAGAGCTTGGCTTGGAGAAGGGTTGGGGTGACA	
Sus1	(720)	ATTTCAACACAGGTTCCAGGAACCTTGGTCTGGAGAAGGGTTGGGGTGATT	
Sus3	(658)	ATTTGCTTATAAATTTCAAGAGTGGGGCCTGGAGAAAGGTTGGGGTGATA	
Consensus	(751)	ATTT ACCATAGGTTCCAAGAGCTTGGCCTGGAGAAGGGTTGGGGTGATA	
		801	850
Sh1	(790)	CTGCGAAGCGTGTCTCTGACACACTCCACTTGCTTCTCGACCTTCTTGAG	
Sus1	(770)	GCGCTAAGCGTGACAGGAGACTATCCACCTCCTCTTGGACCTCCTTGAG	
Sus3	(708)	CAGCAGGACATGTTTTGGAAATGATCCATCTCCTTCTAGACATCATTGAG	
Consensus	(801)	C GC AAGCGTGTCTGGA AC ATCCACCTCCTTCT GACCTCCTTGAG	
		851	900
Sh1	(840)	GCCCCTGATCCTGCCAAGCTTGGAGAAGTTTCTTGGAACCTATACCAATGAT	
Sus1	(820)	GCCCCAGATCCGTCCACCCTGGAGAAGTTTCTTGGAACGATCCCCATGGT	
Sus3	(758)	GCGCCAGACCCATCTACCCTAGAGAAATTCTTGGGGAGGATCCCCATGAT	
Consensus	(851)	GCCCCAGATCC TCCACCCTGGAGAAGTTTCTTGGAACGATCCCCATGAT	
		901	950
Sh1	(890)	GTTCAACGTTGTTATCCTGTCTCCTCATGGCTACTTCGCCCAGTCCAATG	
Sus1	(870)	GTTCAATGTGTTATCCTCTCCCCCTCATGGTACTTCGCTCAAGCTAATG	
Sus3	(808)	TTTTAACGTTGTTGTTGTTATCCCCCTCATGGATACTTTGGTCAAGCTAATG	
Consensus	(901)	GTTCAACGTTGTTATCCT TCCCCCTCATGG TACTTCGCTCAAGCTAATG	
		951	1000
Sh1	(940)	TGCTTGGATACCCTGACACTGGCGGTGAGGTTGTGTACATTCTGGATCAA	
Sus1	(920)	TCTTGGGTTACCCTGACACCGGAGGCCAGGTTGTGTACATCTTGGATCAA	
Sus3	(858)	TATTAGGCTTGCCAGACACAGGAGGACAGATCGTCTATATACTGGACCAA	
Consensus	(951)	T TT GG TACCCTGACAC GGAGG CAGGTTGTGTACAT CTGGATCAA	
		1001	1050
Sh1	(990)	GTCCGTGCTTTGGAGAATGAGATGCTTCTGAGGATTAAGCAGCAAGGCCCT	
Sus1	(970)	GTGCGCGCTATGGAGAAAGAAATGCTGCTGAGGATCAAGCAGTGTGGTCT	
Sus3	(908)	GTCCGTGCACTAGAAAATGAGATGGTCTCCGTTTAAAGAAACAAGGGCT	
Consensus	(1001)	GTCCGTGCT TGGAGAATGAGATGCTTCTGAGGAT AAGCAGCAAGG CT	

Figure 9b

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		1051	1100
Sh1	(1040)	TGATATCACTCCGAAGATCCTCATTGTTACCAGGCTGTTGCCTGATGCTG	
Sus1	(1020)	TGACATCACGCCGAAGATCCTTATTGTACCAGGTTGCTCCCTGATGCAA	
Sus3	(958)	TGATGTTTCCCAAAGATTCTCATTGTTACTCGGCTGATACCAGATGCAA	
Consensus	(1051)	TGATATCAC CCGAAGATCCTCATTGTTACCAGGCTG T CCTGATGCAA	
		1101	1150
Sh1	(1090)	CTGGGACTACGTGCGGTCAGCGGCTGGAGAAGGTCATTGGTACTGAGCAC	
Sus1	(1070)	CTGGCACCACCTGTGGCCAGCGCCTTGAGAAGGTCCTTGGCACCAGCAC	
Sus3	(1008)	AAGGAACATCATGCAATCAGCGGCTTGAGAGAATTAGTGGAACACAGCAT	
Consensus	(1101)	CTGG AC AC TCGGTCAGCGGCTTGAGAAGGTCATTGG AC GAGCAC	
		1151	1200
Sh1	(1140)	ACAGACATCATTGCGGTTCCCTTCAGAAATGAGAATGGCATCCTCCGCAA	
Sus1	(1120)	TGCCATATCCTTCGCGTGCCATTGAGAAAGAGAAATCGTTCGCAA	
Sus3	(1058)	ACTTACATATTACGAGTTCCCTTCAGAAATGAAAATGGGATACTTAAGAA	
Consensus	(1151)	AC ACATC TTCGCGTTCCCTTCAGAAATGAAAATGG ATCCTTCGCAA	
		1201	1250
Sh1	(1190)	GTGGATCTCTCGTTTTGATGTCTGGCCATACCTGGAGACATACACTGAGG	
Sus1	(1170)	GTGGATCTCGCGATTTGAAGTCTGGCCGTACCTGGAGACTTACACTGATG	
Sus3	(1108)	ATGGATATCAAGATTTGATGTGTGGCCATATCTGGAAACATTTGCTGAGG	
Consensus	(1201)	GTGGATCTC CGATTTGATGTCTGGCCATACCTGGAGACATACACTGAGG	
		1251	1300
Sh1	(1240)	ATGTTTCAGTGAAATAATGAAAGAAATGCAGGCCAAGCCTGACCTTATC	
Sus1	(1220)	ACGTGGCGCATGAGATTGCTGGAGAGCTTCAGGCCAATCCTGACCTGATC	
Sus3	(1158)	ATGCTGCTGGTGAAATTGCTGCTGAATTACAAGGTACTCCAGACTTCATA	
Consensus	(1251)	ATGTTGC GTGAAATTGCTG AGAA T CAGGCCAATCCTGACCT ATC	
		1301	1350
Sh1	(1290)	ATTGGCAACTACAGCGATGGCAACCTAGTCCGCACTCTGCTCGCGCACAA	
Sus1	(1270)	ATCGGAAACTACAGTGACGGAAACCTTGTTCGCTGTTTGTCTCGCCACAA	
Sus3	(1208)	ATTGGAAACTACAGTGATGGAAATCTTGTGGCGTCATTGCTATCTTACAA	
Consensus	(1301)	ATTGGAAACTACAGTGATGGAAACCTTGT GCGTCTTTGTCTCG CACAA	
		1351	1400
Sh1	(1340)	GTGGGAGTCACTCAGTGTACCATCGCTCATGCCTTGGAGAAAACCAAT	
Sus1	(1320)	GATGGGTGTTACTCACTGTACCATGCCCATGCGCTTGAGAAAACCTAAGT	
Sus3	(1258)	GATGGGAATTACCCAGTGCAACATTGCTCATGCTCTGGAAGGACTAAGT	
Consensus	(1351)	GATGGGAGTTACTCAGTGTACCATGCTCATGC CTGGAGAAAACCTAAGT	
		1401	1450
Sh1	(1390)	ACCCCAACTCGGACATCTACTTGGACAAATTGACAGCCAGTACCACTTC	
Sus1	(1370)	ACCCTAACTCCGACCTCTACTGGAAGAAGTTTGAGGATCACCTACCACTTC	
Sus3	(1308)	ATCCAGATTACAGACATATTTTGAAGAATTTCGATGAGAAAGTACCATTC	
Consensus	(1401)	ACCC AACTC GACATCTACTGGAAGAA TTCGA GA CAGTACCACTTC	
		1451	1500
Sh1	(1440)	TCTTGCCAGTTCACAGCTGACCTTATTGCCATGAACCAACCGATTTCAT	
Sus1	(1420)	TCTTGCCAGTTCACCACTGACTTGATTGCAATGAACCATGCCGACTTCAT	
Sus3	(1358)	TCCTGCCAGTTCAGTCTGATATAATTGCTATGAACAATGCTGATTTTAT	
Consensus	(1451)	TC TGCCAGTTCAC GCTGAC T ATTGC ATGAACCATGCCGATTTCAT	
		1501	1550
Sh1	(1490)	CATCACCAGCACATTCCAAGAAATCGCGGGAAGCAAGGACACCGTGGGGC	
Sus1	(1470)	CATCACCAGTACCTTCCAAGAGATCGCCGGAACAAGGACACCGTCGGCC	
Sus3	(1408)	CATCACCAGCACATACCAAGAAATTGCTGGAAGCAAAAAATACTGTTGGAC	
Consensus	(1501)	CATCACCAGCACATTCCAAGAAATCGC GGAAGCAAGGACACCGT GG C	

Figure 9c

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		1551	1600
Sh1	(1540)	AGTACGAGTCCCATATCGCGTTCACTCTTCCTGGGCTCTACCGTGTCTGTC	
Sus1	(1520)	AGTACGAGTCACACATGGCGTTCAATGCCTGGCCTGTACCGCGTTGTC	
Sus3	(1458)	AGTATGAGAGTCATACTGCCTTTACTCTGCCTGGTCTGTACCGAGTTGTC	
Consensus	(1551)	AGTACGAGTC CATAT GCGTTCACTCTGCCTGG CTGTACCG GTTGTC	
		1601	1650
Sh1	(1590)	CATGGCATCGATGTTTTCGATCCCAAGTTCAACATTTGTCTCTCCTGGAGC	
Sus1	(1570)	CACGGCATTTGATGTGTTTCGACCCCAAGTTCAACATCGTGTCTCCTGGCGC	
Sus3	(1508)	CATGGGATCGATGTTTCGATCCCAAGTTCAATATAGTCTCTCCTGGAGC	
Consensus	(1601)	CATGGCATCGATGT TTCGATCCCAAGTTCAACAT GTCTCTCCTGGAGC	
		1651	1700
Sh1	(1640)	AGACATGAGTGTTTACTACCCCTTATACGGAAACGACAAGAGACTCACTG	
Sus1	(1620)	GGACCTGTCCATCTACTTCCCGTACACCGAGTCGCACAAGAGGCTGACCT	
Sus3	(1558)	TGACATGTCCATATACTTTCCACATAACCGAGAAGGCCAAGCGACTCACCT	
Consensus	(1651)	GACATGTCCAT TACTTCCC TATACCGAGACGGACAAGAGACTCACCT	
		1701	1750
Sh1	(1690)	CCTTCCATCCTGAAATCGAGGAGCTCATCTACAGCGACGTCGAGAACTCC	
Sus1	(1670)	CCCTTCACCCGGAGATTGAGGAGCTCCTGTACAGCCAAACCGAGAACACG	
Sus3	(1608)	CTCTTCATGGTTCAATCGAAAATTTGATTTATGACCCGGAGCAAACGAT	
Consensus	(1701)	CCCTTCATCCTGAAATCGAGGAGCTCAT TACAGCCA G CGAGAAC C	
		1751	1800
Sh1	(1740)	GAGCACAAGTTCGTGCTGAAGGACAAGAAGAAGCCGATCATCTTCTCGAT	
Sus1	(1720)	GAGCACAAGTTCGTTCTGAACGACAGGAACAAGCCAATCATCTTCTCCAT	
Sus3	(1658)	GAACACATTGGGCATCTGGATGACCGGTCAAAGCCCATCTCTTCTCCAT	
Consensus	(1751)	GAGCACAAGTTCGTTCTGAA GACAGGAA AAGCC ATCATCTTCTCCAT	
		1801	1850
Sh1	(1790)	GGCGCGTCTCGACCGCGTGAAGAACATGACAGGCCTGGTCGAGATGTACG	
Sus1	(1770)	GGCTCGTCTCGACCGGTGTGAAGAACTTGACTGGGCTGGTGGAGCTGTACG	
Sus3	(1708)	GGCAAGACTCGACAGGGTGAAGAACATAACAGGGCTGGTCTGAAGCTTTTG	
Consensus	(1801)	GGC CGTCTCGACCG GTGAAGAACATGACAGGGCTGGTCGAG TGTACG	
		1851	1900
Sh1	(1840)	GCAAGAACGCGCGCTGAGGGAGCTGGCGAACCTCGTGATCGTTGCCGGT	
Sus1	(1820)	GCCGGAACAAGCGGCTGCAGGAGCTGGTGAACCTCGTGGTCTGTGCGGC	
Sus3	(1758)	CTAAGTGCCTAAGCTGAGGGAGCTGGTAAACCTTGTCTGCTGTTGCCGGG	
Consensus	(1851)	GCAAGAACGCGCGGCTGAGGGAGCTGGTGAACCTCGTGGTCTGTGCCGG	
		1901	1950
Sh1	(1890)	GACCACGG ---CAAGGAGTCCAAGGACAGGGAGGAGCAGGCGGAGTTCAA	
Sus1	(1870)	GACCATGG ---CAACCCTTCCAAGGACAAGGAGGAGCAGGCCGAGTTCAA	
Sus3	(1808)	TACAATCATGTCAACAAGTCCAAGGACAGGGAAGAGATCGCGGAGATAGA	
Consensus	(1901)	GACCATGG CAAC AGTCCAAGGACAGGGAGGAGCAGGCGGAGTTCAA	
		1951	2000
Sh1	(1937)	GAAGATGTACAGCCTCATCGACGAGTACAAGTTGAAGGGCCATATCCGGT	
Sus1	(1917)	GAAGATGTTTGACCTCATCGAGCAGTACAACCTGAACGGGACATCCGCT	
Sus3	(1858)	GAAGATGCATGAATCATCAAGACCCACAACCTTGTTCCGGGCGATTCCGCT	
Consensus	(1951)	GAAGATGTATGACCTCATCGAG AGTACAACCTGAACGGGCA ATCCGCT	
		2001	2050
Sh1	(1987)	GGATCTCGGCGCAGATGAACCGTGTCGCAACGGGGAGCTGTACCGCTAC	
Sus1	(1967)	GGATCTCGGCCAGATGAACCGCGTCCGCAACGGCGAGCTGTACCGCTAC	
Sus3	(1908)	GGATCTCTGCCAGACAAACAGGGCCGTAACGGCGAGCTCTATCGCTAC	
Consensus	(2001)	GGATCTC GCCCAGATGAACCG GTCCGCAACGGCGAGCTGTACCGCTAC	
		2051	2100
Sh1	(2037)	ATTTGCGATACCAAGGGCGCATTTCGTGCAGCCTGCGTTCTACGAAGCGTT	
Sus1	(2017)	ATCTGCGACACCAAGGGCGCCTTCGTGCAGCCTGCTTTCTACGAGGCTTT	
Sus3	(1958)	ATCGCTGATACCCATGGTGCTTTTCGTACAGCCGGCCTTGATGAAGCGTT	
Consensus	(2051)	ATCTGCGATACCAAGGGCGC TTCGTGCAGCCTGC TTCTACGAAGCGTT	

Figure 9d

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		2101	2150
Sh1	(2087)	CGGCCTGACTGTGATCGAGTCCATGACGTGCGGTCTGCCAACGATCGCGA	
Sus1	(2067)	CGGGCTGACGGTGGTTGAGGCCATGACCTGCGGCCTGCCACGTTTCGCCA	
Sus3	(2008)	CGGTCTCACCCTCGTTGAGGCCATGACCTGTGGGCTTCCTACTTTTCGCGA	
Consensus	(2101)	CGG CTGAC GTGGTTGAGGCCATGACCTGCGG CTGCC ACGTTTCGCGA	
		2151	2200
Sh1	(2137)	CCTGCCATGGCGGCCCTGCTGAGATCATCGTGGACGGGGTATCTGGCCTG	
Sus1	(2117)	CCGCCTACGGCGGTCCGGCCGAGATCATCGTGACGGCGTGTCTGGCTAC	
Sus3	(2058)	CGCTCCATGGAGGTCCAGCTGAGATCATAGAGCATGGCGTCTCGGGCTTC	
Consensus	(2151)	CC CCATGGCGGTCC GCTGAGATCATCGTGACGGCGT TCTGGCTTC	
		2201	2250
Sh1	(2187)	CACATTGACCCTTACCACAGCGACAAGGC GCGGATATCTGGTCAACTT	
Sus1	(2167)	CACATCGACCCTTACCAGGGCGACAAGGCGTGGGCCCTGCTCGTGGACTT	
Sus3	(2108)	CACATTGACCCTTACCACCCGACAGGCTGTTAATCTGATGGCCGACTT	
Consensus	(2201)	CACATTGACCCTTACCAC GCGACAAGGC GCGGATCTGCTGGTTCGACTT	
		2251	2300
Sh1	(2237)	CTTTGACAAATGCAAGGCAGATCCGAGCTACTGGGACGAGATCTCACAGG	
Sus1	(2217)	CTTCGACAAGTGCCAGGCGGAGCCGAGCCACTGGAGCAAGATCTCCAGG	
Sus3	(2158)	CTTCGACCCTGCAAGCAAGACCCAGATCACTGGGTGAATATATCTGGAG	
Consensus	(2251)	CTTCGACAAGTGCAAGGCAGA CCGAGCCACTGGG CAAGATCTC CAGG	
		2301	2350
Sh1	(2287)	GCGGCCTGCAGAGAATTTATGAGAAGTACACCTGGAAGCTCTACTCCGAG	
Sus1	(2267)	GCGGGCTCCAGCGTATCGAGGAGAAGTACACCTGGAAGCTGTACTCCGAG	
Sus3	(2208)	CAGGGCTGCAGCGCATATACGAGAAGTACACATGGAAGATATACTCAGAG	
Consensus	(2301)	GCGGGCTGCAGCG AT TA GAGAAGTACACCTGGAAGCT TACTC GAG	
		2351	2400
Sh1	(2337)	AGGCTGATGACCCTGACCGGCGTGTACGGGTTCTGGAAGTACGTGAGCAA	
Sus1	(2317)	AGGCTGATGACCCTCACCGGCGTGTACGGGTTCTGGAAGTACGTGTCAA	
Sus3	(2258)	AGGTTGATGACACTGGCCGGGGTCTACGGTTCTGGAAGTACGTGTCAA	
Consensus	(2351)	AGGCTGATGACCCTGACCGGCGTGTACGGGTTCTGGAAGTACGTGTCAA	
		2401	2450
Sh1	(2387)	CCTGGAGAGGCGCGAGACCCGCGCTACATCGAGATGTTCTACGCCCTGA	
Sus1	(2367)	CCTGGAGAGGCGCGAGACCCGGCGGTACCTGGAGATGCTGTACGCCCTCA	
Sus3	(2308)	GCTCGAGAGGCTGGAGACGAGGCGCTACCTTGAGATGTTCTACATACTGA	
Consensus	(2401)	CCTGGAGAGGCGCGAGACCCGGCGCTACCT GAGATGTTCTACGC CTGA	
		2451	2500
Sh1	(2437)	AGTACCGTAGCCTGGCAAGCCAGGTTCCGCTGTCTTTCGA-----TTAG	
Sus1	(2417)	AGTACCGCACCATGGCGAGCACCGTGCCGCTGGCCGTGGA-----GGGA	
Sus3	(2358)	AGTTCCGCGAGCTGGCGAAGACCGTGCCGCTTGCAATTGACCAACCGCAG	
Consensus	(2451)	AGTACCGCA CCTGGCGAGCACCGTGCCGCTGGCC T GA G AG	
		2501	2550
Sh1	(2481)	TACGGGGAAAGAAGGAGA-AGAAGAAGAAGAAGCCAGGCCGGA-----G	
Sus1	(2461)	GAGCCCTCCAGCAAGTGA-TGCGTGACGGCGGCCACAGACCTGATC---G	
Sus3	(2408)	TAGCTTGCGCAACTGCGACTGCGTAGCACTTGGTACAAGACTGAAACCTG	
Consensus	(2501)	TAGC GC AGAA G GA TGCCTAACA GGCACAGGCCTGA G	
		2551	2600
Sh1	(2525)	AACCATCGCCTGCATTTTCGATCT-----GT-TTCACCGCAATTCGC	
Sus1	(2507)	ATCGATGAGCGAGAGGGAGCACTCGGA-----GT-GTCGTGTCTTTTCC	
Sus3	(2458)	AAGGACCTTCAGTAATTTAGGCGCGGAGACGGTAGCCAATAAATGTGC	
Consensus	(2551)	AACGATC C G A TT G CTCGG GT GTCA CAATTCGC	

Figure 9e

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2601                                                    2650
Sh1 (2565) ATTGTTAGTCGTGTATTGGAGTTATGTG--TACTTGGTTTCCAAGAACTT
Sus1 (2551) TTGCCATTTCTTTCTTTCTTTCTTTTCC--TTCCCGGAGGCCGAAAAAAA
Sus3 (2508) CGGAGCTGAACCTGGTTTTTTTATTATGTACATAATGGCAGTATAACAAAAT
Consensus (2601) TG TGTC TG TTT TT TTATGT TACT GGAGTC AA AAAAT

2651                                                    2700
Sh1 (2613) TGGTTCCTTCTCGTTTTTTTTTCTTGTGTTTGAGCGTTTTTGGGCAGCGCTG
Sus1 (2599) AGAGTC-TGCTT-TTGCTAGGCGGCGGGCGTTTCGTTGCTGCTCTTTGCTT
Sus3 (2558) TACTGAAGGCAGGTGGGTTGCAGTTGTGTGTTTCGTTACTG-----TT
Consensus (2651) TG TTC TGCT GTTG TTG CGTTGTGTGTTTCGTT CTG C GCT

2701                                                    2750
Sh1 (2663) GCCTGGTTCCTAGTATGGTGGGAATTGGCTGCACCTTTTGCTTCGAATAA
Sus1 (2647) CAAGAGTTAAAATTTACCTACC--TTGTCAAGGTCTTGTTCATCATGA
Sus3 (2600) TACTGTATTATGTCAAGCTGTC---GGCTGCAATTTCTTTGCTGG--CA
Consensus (2701) ACTGGTT ATATTAAGCTG C TTGGCTGCA CTT TTC TGA T A

2751                                                    2800
Sh1 (2713) AAATGCCTGCTCGTTTCACCTGTCTTCCAGAGTGC-----
Sus1 (2695) TCCGGGTGTCTGCTTGTAGTAGTCTGATGGACTGTTAGTAGTTTTCGTTGC
Sus3 (2644) AGCCGCAGGCACTGGTGAAGTGCTGATAAATACATCATATTTCTGTTGACC
Consensus (2751) A C GC GGC CTTGTA GTCTGATAGA TG T TA T TG C

2801                                                    2850
Sh1 (2747) -----
Sus1 (2745) GTCGGTTGAGAGGGAACGTTGGTGGTGGTGGTGTGTGTGCAGTCAGGCGT
Sus3 (2694) TGTGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC-----
Consensus (2801) G A A AA G G G C

2851                                                    2900
Sh1 (2747) -----
Sus1 (2795) GGTGCTCCCTTTGTTTCTGGATGGGATGTTGCTCCTTGAATAATAATCG
Sus3 (2738) -----
Consensus (2851)

2901                                                    2950
Sh1 (2747) -----
Sus1 (2845) TAGTGGCCTTGGAGCCCTTTTCTGAAATAAGAGCAGCATCCTAGTGCTT
Sus3 (2738) -----
Consensus (2901)

2951 2964
Sh1 (2747) -----
Sus1 (2895) ACCTTTGCAGCTGT
Sus3 (2738) -----
Consensus (2951)

```

Figure 9f

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CGCCAGTCGCCAGTCGCCACAGCCACACCACACCACACTAGCCGCGGCCGCGGGTAGGAG
CGCGCGCGGCGCGGGCGGAACGACCCACCGGTGGCGGCAGCCATGTCTGCCCCGAAGCTGA
ACCGCAACGCGAGCATCCGGGACCGCGTCGAGGACACCCTCCACGCGCACCGCAACGAGC
TCGTCGCCCTCCTCTCCAAGTACGTGAACAAGGGGAAGGGCATCCTGCAGCCGCACCACA
TCCTCGACGCGCTCGACGAGGTCCAGGGCTCCGGGGTCCGCGCGCTCGCCGAGGGACCCT
TCCTCGACGTCCTCCGCTCCGCGCAGGAGGCGATCGTGCTGCCGCCG

Figure 10

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Sorghum sequence from SEQ ID NO: 13 in SEQ ID NO: 11
ATGTCGCCCCGAAGCTGAACCGCAACGCGAGCATCCGG

Maize sequence from SEQ ID NO: 1 in SEQ ID NO: 11

gtcgacccac gagtegggg	accgcgctcga	ggacaccctc	cacgcgcacc	gcaacgagct	60
cgtcgcccctc	ctgtccaagt	acgtgaacaa	gggggaagggc	atcctgcagc	120
cctcgacgcg	ctcgacgagg	tccagggctc	cggggggccgc	gcgctagccg	180
cctcgacgctc	ctccgctccg	cgcaggaggc	gatcgtgctg	ccgccgttcg	240
ggtgcgcccc	cgcccgggag	tttgggagta	cgcccgcgtc	aacgttcacg	300
cgagcagctc	acagtctcgg	agtacctccg	cttcaaggag	gagcttgctg	360
caatgatccc	tacgttctcg	agcttgactt	cgagccgttc	aatgtctcag	420
aaatcgggtca	tcatctattg	gaaacgggtg	gcagttcctc	aaccgacact	480
catgtttccgc	aacagggatt	gcttgaggcc	cctgttggat	ttcctccgtg	540
caagggggcat	ggtatgatgc	ttaatgatag	aatacaaaagc	ttggggaggc	600
gctgacccaaa	gctgaggagc	acttgtcaaa	gtccccgtct	gacacacat	660
tgcttataaaa	tttcaagagt	ggggcctgga	gaaagggttg	ggtgatacag	720
tttggaaatg	atccatctcc	ttctagacat	cattcaggcg	ccagacccat	780
gaaattcttg	gggaggatcc	ccatgatttt	taacgttggt	gtggtatccc	840
ctttgggtcaa	gctaattgtat	taggcttgcc	agacacagga	ggacagatcg	900
ggaccaagtc	cgtgcactag	aaaatgagat	ggttctccgt	ttaaagaaac	960
tgtttcccca	aagattctca	ttgttactcg	gctgatacca	gatgcaaaag	1020
caatcagcgg	cttgagagaa	ttagtggaa	acagcatact	tacataattac	1080
cagaaatgaa	aatgggatac	ttaagaaatg	gatatacaaga	tttgatgtgt	1140
ggaaacattt	gctgaggatg	ctgctggtga	aattgctgct	gaattacaag	1200
cttcataatt	ggaaactaca	gtgatggaaa	tcttggtggc	tcattgctat	1260
gggaattacc	cagtgcacaa	ttgctcatgc	tctggaaaag	actaagtatc	1320
catatttttg	aagaatttctg	atgagaagta	ccattttctc	tgccagttca	1380
aattgctatg	aacaatgctg	attttatcat	caccagcaca	taccaagaaa	1440
caaaaatact	gttgagacag	atgagagtca	tactgccttt	actctgcctg	1500
agttgtccat	gggactgatg	tcttcgatcc	aaagttcaat	atagtctctc	1560
catgtccata	tactttccac	ataccgagaa	ggccaagcga	ctcacctctc	1620
aatcgaaaat	ttgatttatg	acccggagca	aaacgatgaa	cacattgggc	1680
ccggtcaaa	cccatcctct	tctccatggc	aagactcgac	agggatgaaga	1740
gctgggtcgaa	gcttttgcta	agtgcgctaa	gctgagggag	ctggtaaacc	1800
tgccgggtgac	aatgatgtca	acaagtccaa	ggacagggaa	gagatcgcg	1860
gatgcatgaa	ctcatcaaga	cccacaactt	gttcgggcag	ttccgctgga	1920
gacaaacagg	gcccgtaacg	gcgagctcta	tcgctacatc	gctgataccc	1980
cgtacagccg	gccttgatg	aagcgttcgg	tctcaccgtc	gttgaggcca	2040
gcttccctact	ttcgcgacgc	tccatggagg	tccagctgag	atcatagagc	2100
gggcttccac	attgacccgt	accaccccga	acaggctggt	aatctgatgg	2160
cgaccgggtgc	aagcaagacc	cagatcactg	ggtgaatata	tctggagcag	2220
catatacgag	aagtacacat	ggaagatata	ctcagagagg	ttgatgacac	2280
ctacgggtttc	tggaagtacg	tgctgaagct	cgagaggctg	gagacgaggc	2340
gatgtttctac	atactgaagt	tccgcgagct	ggcgaagacc	gtgccgcttg	2400
accgcagtag	cttgcgcaac	tgcgactgcg	tagcacttgg	tacaagactg	2460
gaccttcagt	aatttaggcg	cggcagacgg	tagccaataa	aatgtgccgg	2520
gttttttatt	atgtacataa	tggcagatata	acaaaattac	tgaaggcagg	2580
ttgtgtgttc	gttactgttt	actgtattat	gtcaagctgt	cggctgcaat	2640
gcaagccgca	ggcactgggtg	aagtgtctgat	aaatacatca	tattctgttg	2700
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaggg	cggccgcg		

Figure 11